TABLE S1: The oligonucleotide primers used for the real-time qPCR

Genes	Primer sequences
ef1α	5'-CGTGGTAATGTGGCTGGAGA
	5'-CTGAGCGTTGAAGTTGGCAG
fbp1a	5'-ATCGTTGTAGAGCCAGATAGAC
	5'-TGTAGATGGCAAAGATGGTCC
gclm	5'-ATCCATCAGAAGTGCGGTAG
	5'-AGTGTCTGGCTTTCACCCTC
gsr	5'-CAGATTTACAGGAGCAACCTTG
	5'-TGACTTCAACTGTGGGTTCAG
gsto2	5'-ATGGCTTCATCTCCAAAATGC
	5'-AGGGCAGAATCTCATGCTGTAG
gstp1	5'-CAACGCCATGCTGAGACATC
	5'-GAAGATCTTCAACGCCGTCG
keap1a	5'-ATACCAACCAGACACCAACAC
	5'-GGTTTGTCCATCATAGCCTCC
nrf2a	5'-ATGTCTAAAATGCAGCCAAGCC
	5'-CGGTAGCTGAAGTCGAACAC
pck1	5'-GGAGAACAGCACCATCCTCAG
	5'-AGTCGGTGTGGGAACCGTG
pcxb	5'-AGATGGGGGATAAAGTGGAAG
	5'-TCTTGAAGGCATGAGATAGGAG
pgd	5'-TGGAATACGGCACACCTGTC
	5'-AGGCTCTTACTGGCCTGAAC
psma3	5'-ACGGAAGGGTATTTCAGGTTG
	5'-TCATACAGCTTGGACAGTACC
psma5	5'-AGTAAACACTTTCTCACCAGAAG
	5'-TCTCCACAGCAAGACAAACTC
psmb7	5'-GAGCTTCATTCTCTGTCCACC
	5'-GCAATCGACACCTCCAAGAAC
sqstm1	5'-TTGGCTCTTGTGAAGGATGAC
	5'-TGTAGTGAACGGAAACCCAGG
taldo1	5'-TCTGTATCACCGGACAAACG
	5'-TCCTGAGGCTTGTACTCTTC

TABLE S2: The oligonucleotide primers used for plasmid construction

Plasmids	Primer sequences
pKSpsma3	5’-GGGGGATCCTGATCGCAGTGACTTAAAATG
	5’-GGGCTCGAGACATGTTGTCCTCATCAGAGTC
pKSpsma5	5’-GGGGAATTCTCCACTGCAGAAGATTTGCG
	5’-GGGCTCGAGAGCACGTTTAGATATCCTTGATG
pKSpsmb7	5’-GGGGGATCCAGACCGCAGAATCATGGCGAC
	5’-GGGCTCGAGTCTTGTTGGCAATGTCGTGAG
pKSpgd	5’-GGGGGATCCAGCAGTCAAAACCCTCATCG
	5’-GGGCTCGAGCATTTCCCTGTGCCCTTCTG
pKSfbp1a	5’-GGGGGATCCGATGGTTCATCCAACATTGAC
	5’-GGGCTCGAGGGCATCTTATTCTGGAGTGTC

TABLE S3: The genes induced by the overexpression of *nrf2a* in zebrafish.

Ratio	Gene symbol in ZFIN (or [19])	Gene product	Refs.	
			microarray	confirmd by PCR
9.96	*gclm*	glutamate-cysteine ligase, modifier subunit	[19,20]	[19]
7.34	*hmox1a*	heme oxygenase 1a	–	[19]
6.53	*pimr138*	Pim proto-oncogene, serine/threonine kinase, related 138	–	–
5.81	*aifm4*	apoptosis-inducing factor, mitochondrion-associated, 4	[19,20]	–
5.71	*gstp1*	glutathione *S*-transferase pi 1	[19]	[11,16,17,19]
4.50	*txn*	thioredoxin	[19,20]	[16]
4.02	*zp2l1*	zona pellucida glycoprotein 2, like 1	–	–
3.83	*zgc:92066* (*fthl*)	ferritin heavy chain like	[19,20]	[19]
3.39	*tex2*	testis expressed 2	[19]	–
3.21	*gsto2*	glutathione *S*-transferase omega 2	[19]	–
2.98	*gclc*	glutamate-cysteine ligase, catalytic subunit	[20]	[16,17,19]
2.84	*pcxb*	pyruvate carboxylase b	[19]	–
2.70	*exorh*	extra-ocular rhodopsin	–	–
2.65	*zfand2a*	zinc finger, AN1-type domain 2A	–	–
2.49	*ugdh*	UDP-glucose 6-dehydrogenase	[19]	–
2.47	*mgst3b*	microsomal glutathione *S*-transferase 3b	[19,20]	[19]
2.37	*sepw2b*	selenoprotein W, 2b	[19]	[19]
2.36	*pisd*	phosphatidylserine decarboxylase	–	–
2.33	*lgals2a*	lectin, galactoside-binding, soluble, 2a	–	–
2.32	*cbr1l*	carbonyl reductase 1-like	[19]	–
2.25	*lrrc6*	leucine rich repeat containing 6	–	–
2.25	*tjp2b*	tight junction protein 2b (zona occludens 2)	–	–
2.13	*sqrdl*	sulfide quinone reductase-like (yeast)	[19]	–
2.13	*spata6l*	spermatogenesis associated 6-like	–	–
2.11	*sec23b*	Sec23 homolog B, COPII coat complex component	–	–
2.11	*slc40a1*	solute carrier family 40 (iron-regulated transporter), member 1	–	–
2.09	*rab43*	RAB43, member RAS oncogene familly	[19]	–
2.08	*sqstm1*	sequestosome 1	[20]	–
2.07	*lmo7a*	LIM domain 7a	–	–
2.06	*hsp90aa1.1*	heat shock protein 90, alpha (cytosolic), class A member 1, tandem duplicate 1	–	–
2.00	*keap1a*	kelch-like ECH-associated protein 1a	[20]	–
2.00	*fam13b*	family with sequence similarity 13, member B	–	–
1.94	*tradd*	tnfrsf1a-associated via death domain	–	–
1.94	*ctsk*	cathepsin K	–	–
1.94	*selp*	selectin P	–	–
1.92	*tpk1*	thiamin pyrophosphokinase 1	–	–
1.91	*rsrp1*	arginine/serine-rich protein 1	[20]	–
1.87	*gsta.1* (*gstal*)	glutathione *S*-transferase, alpha tandem duplicate 1	[19]	[19]
1.87	*epoa*	erythropoietin a	–	–
1.85	*pfas*	phosphoribosylformylglycinamidine synthase	–	–
1.85	*setdb1a*	SET domain, bifurcated 1a	–	–

Gray highlighting indicate genes that were also identified in the previous microarray analyses using DEM- or tBHQ-treated larvae [19,20].

TABLE S3: The genes induced by the overexpression of *nrf2a* in zebrafish. (continued)

Ratio	Gene symbol in ZFIN (or [19])	Gene product	Refs.	
			microarray	confirmd by PCR
1.84	*apoa1a*	apolipoprotein A-Ia	–	–
1.83	*gpx1b*	glutathione peroxidase 1b	–	–
1.80	*pik3c2a*	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha	–	–
1.80	*psma3*	proteasome subunit alpha 3	–	–
1.78	*cyp2r1*	cytochrome P450, family 2, subfamily R, polypeptide 1	–	–
1.78	*si:dkey-33c12.4*	tetratricopeptide repeat domain 31 (ttc31) (ENSDARG00000057890)	–	–
1.78	*esrp1*	epithelial splicing regulatory protein 1	–	–
1.78	*si:ch211-95j8.2*	claudin 23 like (ENSDARG00000028096)	–	–
1.78	*coa3a*	cytochrome C oxidase assembly factor 3a	–	–
1.72	*epn2*	epsin 2	–	–
1.72	*brf1a*	BRF1, RNA polymerase III transcription initiation factor a	–	–
1.71	*col4a1*	collagen, type IV, alpha 1	–	–
1.71	*ndrg3a*	ndrg family member 3a	–	–
1.69	*tp53bp2a*	tumor protein p53 binding protein, 2a	–	–
1.68	*cxcr4b*	chemokine (C-X-C motif), receptor 4b	–	–
1.68	*phyh*	phytanoyl-CoA 2-hydroxylase	–	–
1.68	*nudc*	nudC nuclear distribution protein	–	–
1.68	*gldc*	glycine dehydrogenase (decarboxylating)	–	–
1.68	*taldo1*	transaldolase 1	–	–
1.67	*si:dkey-122c11.8*	novel gene, “zinc finger protein”	–	–
1.67	*anxa1a*	annexin A1a	–	–
1.66	*zgc:163022* (*frrs1c*)	ferric-chelate reductase like (CABZ01041812.1)	[19]	[19]
1.66	*dnase1l3*	deoxyribonuclease I-like 3	–	–
1.65	*atp2b2*	ATPase, Ca^{++} transporting, plasma membrane 2	–	–
1.63	*rbm24a*	RNA binding motif protein 24a	–	–
1.62	*uqcrq*	ubiquinol-cytochrome c reductase, complexIII subunit VII	–	–
1.62	*rab3il1*	RAB3A interacting protein (rabin3)-like 1	–	–
1.62	*sst6*	somatostatin 6	–	–
1.62	*myh9a*	myosin, heavy chain 9a, non-muscle	–	–
1.61	*kpna1*	karyopherin alpha 1 (importin alpha 5)	–	–
1.60	*pck1*	phosphoenolpyruvate carboxykinase 1 (soluble)	[19]	–
1.60	*psma5*	proteasome subunit alpha 5	–	–
1.60	*prdx5*	peroxiredoxin 5	–	–
1.60	*gpx1a*	glutathione peroxidase 1a	–	–
1.59	*lmna*	lamin A	–	–
1.57	*tmem106a*	transmembrane protein 106A	–	–
1.57	*gramd1c*	GRAM domain containing 1c	–	–
1.57	*si:ch211-106h4.6*	novel gene, “plexin domain containing like”	–	–
1.57	*hoxb6b*	homeobox B6b	–	–
1.56	*srprb*	signal recognition particle receptor, B subunit	–	–

Gray highlighting indicate genes that were also identified in the previous microarray analyses using DEM- or tBHQ-treated larvae [19,20].

TABLE S3: The genes induced by the overexpression of *nrf2a* in zebrafish. (continued)

Ratio	Gene symbol in ZFIN (or [19])	Gene product	Refs.	
			microarray	confirmd by PCR
1.55	*slx4*	SLX4 structure-specific endonuclease subunit homolog (*S. cerevisiae*)	–	–
1.55	*gsr*	glutathione reductase	[20]	–
1.55	*ftr82*	fin TRIM family, member 82	–	–
1.55	*map1b*	microtubule-associated protein 1B	–	–
1.55	*prkcdb*	protein kinase C, delta b	[19]	–
1.55	*pth1ra*	parathyroid hormone 1 receptor a	–	–
1.55	*calm3a*	calmodulin 3a (phosphorylase kinase, delta)	–	–
1.55	*gatm*	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	–	–
1.54	*smc5*	structural maintenance of chromosomes 5	–	–
1.54	*caska*	calcium/calmodulin-dependent serine protein kinase a	–	–
1.54	*opn1mw1*	opsin 1 (cone pigments), medium-wave-sensitive, 1	–	–
1.54	*lcp1*	lymphocyte cytosolic protein 1 (L-plastin)	–	–
1.54	*aoc2*	amine oxidase, copper containing 2	[19]	–
1.54	*epb41l5*	erythrocyte membrane protein band 4.1 like 5	–	–
1.54	*tacc2*	transforming, acidic coiled-coil containing protein 2	–	–
1.53	*rbm24a*	RNA binding motif protein 24a	–	–
1.52	*prkacab*	protein kinase, cAMP-dependent, catalytic, alpha, genome duplicate b	–	–
1.52	*runx1t1*	runt-related transcription factor 1; translocated to, 1(cyclin D-related)	–	–
1.52	*gmeb1*	glucocorticoid modulatory element binding protein 1	–	–
1.52	*ctsh*	cathepsin H	–	–
1.52	*sult6b1*	sulfotransferase family, cytosolic, 6b, member 1	[19]	–
1.52	*fbp1a*	fructose-1,6-bisphosphatase 1a	–	–
1.51	*pgd*	phosphogluconate dehydrogenase	[19,20]	–
1.51	*slc4a2a*	solute carrier family 4 (anion exchanger), member 2a	–	–
1.50	*ppiaa*	peptidylprolyl isomerase Aa (cyclophilin A)	–	–
1.50	*zyx*	zyxin	–	–
1.50	*rabif*	RAB interacting factor	–	–
1.50	*acss1*	acyl-CoA synthetase short-chain family member 1	–	–
1.50	*si:ch211-87h14.3*	chromosome 19 open reading frame 60 (C19orf60)	–	–
1.50	*psmb7*	proteasome subunit beta 7	–	–
1.50	*penkb*	proenkephalin b	–	–
1.50	*sepsecs*	Sep (O-phosphoserine) tRNA: Sec (selenocysteine) tRNA synthase	–	–
1.50	*atp6v0a1a*	ATPase, H+ transporting, lysosomal V0 subunit a1a	–	–
1.50	*prdx1*	peroxiredoxin 1	[19,20]	[16,17,19]

Gray highlighting indicate genes that were also identified in the previous microarray analyses using DEM- or tBHQ-treated larvae [19,20].

TABLE S4: The genes repressed by the overexpression of *nrf2a* in zebrafish.

Ratio	Gene symbol in ZFIN	Gene product
0.31	*ccnc*	cyclin C
0.40	*prkacbb*	protein kinase, cAMP-dependent, catalytic, beta b
0.48	*dynll2a*	dynein, light chain, LC8-type 2a
0.51	*slco1f1*	solute carrier organic anion transporter family, member 1F1
0.54	*ipo7*	importin 7
0.55	*tmem135*	transmembrane protein 135
0.56	*hesx1*	HESX homeobox 1
0.57	*vps51*	vacuolar protein sorting 51 homolog (*S. cerevisiae*)
0.57	*cotl1*	coactosin-like F-actin binding protein 1
0.58	*sparc*	secreted protein, acidic, cysteine-rich (osteonectin)
0.58	*phgdh*	phosphoglycerate dehydrogenase
0.59	*sltm*	SAFB-like, transcription modulator
0.60	*pfkpb*	phosphofructokinase, platelet b
0.60	*taf15*	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor
0.60	*kpnb3*	karyopherin (importin) beta 3
0.61	*ncl*	nucleolin
0.61	*efemp2a*	EGF containing fibulin-like extracellular matrix protein 2a
0.62	*srsf5a*	serine/arginine-rich splicing factor 5a
0.62	*rnf19a*	ring finger protein 19A, RBR E3 ubiquitin protein ligase
0.62	*cox15*	cytochrome c oxidase assembly homolog 15 (yeast)
0.63	*fbxo11a*	F-box protein 11a
0.63	*etf1b*	eukaryotic translation termination factor 1b
0.63	*dmrt3a*	doublesex and mab-3 related transcription factor 3a
0.63	*anp32e*	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
0.63	*gnl3*	guanine nucleotide binding protein-like 3 (nucleolar)
0.63	*dennd4c*	DENN/MADD domain containing 4C
0.64	*src*	v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog
0.64	*anos1b*	anosmin 1b
0.64	*pfkfb4b*	6-phosphofructo-2kinase/fructose-2,6-biphosphatase 4b
0.64	*gskip*	gsk3b interacting protein
0.64	*cirbpa*	cold inducible RNA binding protein a
0.64	*sec14l1*	SEC14-like lipid binding 1
0.64	*tcf15*	transcription factor 15 (basic helix-loop-helix)
0.64	*brd2b*	bromodomain containing 2b
0.64	*nudt3a*	nudix (nucleoside diphosphate linked moiety X)-type motif 3a
0.65	*atrx*	alpha thalassemia/mental retardation syndrome X-linked homolog (human)
0.65	*zgc:153953*	chromosome 1 open reading frame 106 (C1orf106)
0.65	*zgc:113452*	novel gene “zink finger protein”
0.65	*kctd4*	potassium channel tetramerization domain containing 4
0.65	*fam60al*	family with sequence similarity 60, member A, like
0.66	*tle2*	transducing-like enhancer of split 2 (E(sp1) homolog, *Drosophila*)
0.66	*mcm6*	minichromosome maintenance complex component 6

TABLE S4: The genes repressed by the overexpression of *nrf2a* in zebrafish. (continued)

Ratio	Gene symbol in ZFIN	Gene product
0.66	*gsna*	gelsolin a
0.66	*snapin*	SNAP-associated protein
0.66	*fscn1a*	fascin actin-bundling protein 1a
0.66	*hoxa10b*	homeobox A 10b
0.67	*bmpr1aa*	bone morphogenetic protein receptor, type IAa
0.67	*stk35*	serine/threonine kinase 35
0.67	*lsm12a*	LSM 12 homolog a
0.67	*tfap2a*	transcription factor AP-2 alpha
0.67	*ptbp1a*	polypyrimidine tract binding protein 1a
0.67	*fzd8a*	frizzled class receptor 8a
0.67	*sema4c*	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain (semaphorin), 4C
0.67	*lrwd1*	leucine-rich repeats and WD repeat domain containing 1
0.67	*supt6h*	SPT6 homolog, histone chaperone